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NOV 23 2001

TECH CENTER 1600/2900

DATE: 11/14/2001

TIME: 13:38:59

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/590,375

Input Set : A:\2173-0120.st25.txt

Output Set: N:\CRF3\11142001\I590375.raw

3 <110> APPLICANT: ENDO, Keiji et al.
 5 <120> TITLE OF INVENTION: MUTANT ALPHA-AMYLASES
 7 <130> FILE REFERENCE: 2173-0120P
 9 <140> CURRENT APPLICATION NUMBER: US 09/590,375
 10 <141> CURRENT FILING DATE: 2000-06-09
 12 <150> PRIOR APPLICATION NUMBER: JP P1999-163569
 13 <151> PRIOR FILING DATE: 1999-06-10
 15 <160> NUMBER OF SEQ ID NOS: 23
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 480
 19 <212> TYPE: PRT
 20 <213> ORGANISM: Bacillus sp. KSM-K38
 22 <400> SEQUENCE: 1
 23 Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu
 5 10 15
 24 Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu
 20 25 30
 25 Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
 35 40 45
 27 Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
 50 55 60
 29 Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
 65 70 80
 31 Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
 85 90 95
 33 Val Tyr Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr
 100 105 110
 35 Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp
 115 120 125
 37 Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser
 130 135 140
 39 Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
 145 150 160
 41 Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg
 165 170 175
 43 Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn
 180 185 190
 45 Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val
 195 200 205
 47 Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp
 210 215 220
 49 Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr
 225 230 240
 51 Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu
 245 250 255
 53 Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe
 260 265 270

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57 Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu
 58 275 280 285
 59 Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Ser Tyr Asp Met
 60 290 295 300
 61 Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala
 62 305 310 315 320
 63 Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu
 64 325 330 335
 65 Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu
 66 340 345 350
 67 Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly
 68 355 360 365
 69 Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu
 70 370 375 380
 71 Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe
 72 385 390 395 400
 73 Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg
 74 405 410 415
 75 Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser
 76 420 425 430
 77 Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp
 78 435 440 445
 79 Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp
 80 450 455 460
 81 Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
 82 465 470 475 480
 85 <210> SEQ ID NO: 2
 86 <211> LENGTH: 485
 87 <212> TYPE: PRT
 88 <213> ORGANISM: Bacillus sp. KSM-AP1378
 90 <400> SEQUENCE: 2
 91 His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His
 92 5 10 15
 93 Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala
 94 20 25 30
 95 Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
 96 35 40 45
 97 Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
 98 50 55 60
 99 Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
 100 65 70 75 80
 101 Thr Arg Ser Gln Leu Gln Gly Ala Val Thr Ser Leu Lys Asn Asn Gly
 102 85 90 95
 103 Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
 104 100 105 110
 105 Gly Thr Glu Met Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn
 106 115 120 125
 107 Gln Glu Ile Ser Gly Glu Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
 108 130 135 140

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109 Phe Pro Gly Arg Gly Asn Thr His Ser Asn Phe Lys Trp Arg Trp Tyr
 110 145 150 155 160
 111 His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys
 112 165 170 175
 113 Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
 114 180 185 190
 115 Ile Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met
 116 195 200 205
 117 Asp His Pro Glu Val Ile Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr
 118 210 215 220
 119 Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
 120 225 230 235 240
 121 Ile Lys Tyr Ser Tyr Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
 122 245 250 255
 123 Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
 124 260 265 270
 125 Ala Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val
 126 275 280 285
 127 Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
 128 290 295 300
 129 Gly Tyr Phe Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys
 130 305 310 315 320
 131 His Pro Ile His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
 132 325 330 335
 133 Gly Glu Ala Leu Glu Ser Phe Val Gln Ser Trp Phe Lys Pro Leu Ala
 134 340 345 350
 135 Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
 136 355 360 365
 137 Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ser Met Lys Ser
 138 370 375 380
 139 Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Tyr Ala Tyr Gly Thr
 140 385 390 395 400
 141 Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
 142 405 410 415
 143 Gly Asp Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
 144 420 425 430
 145 Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys His Lys Ala Gly
 146 435 440 445
 147 Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Ser Gly Thr Val Thr Ile
 148 450 455 460
 149 Asn Ala Asp Gly Trp Gly Asn Phe Thr Val Asn Gly Gly Ala Val Ser
 150 465 470 475 480
 151 Val Trp Val Lys Gln
 152 485
 155 <210> SEQ ID NO: 3
 156 <211> LENGTH: 1753
 157 <212> TYPE: DNA
 158 <213> ORGANISM: Bacillus sp. KSM-K38
 160 <220> FEATURE:

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161 <221> NAME/KEY: sig_peptide
162 <222> LOCATION: (162)..(224)
164 <220> FEATURE:
165 <221> NAME/KEY: mat_peptide
166 <222> LOCATION: (225)..()
168 <220> FEATURE:
169 <221> NAME/KEY: CDS
170 <222> LOCATION: (162)..(1664)
173 <400> SEQUENCE: 3
174 gtatgcgaaa cgatgcgcaa aactgcgcaa ctactagcac tcttcaggga ctaaaccacc      60
176 tttttccaa aaatgacatc atataaacaa atttgtctac caatcactat ttaaagctgt      120
178 ttatgatata tgtaagcggtt atcattaaaa ggaggtatgg g atg aga aga tgg gta      176
179                                         Met Arg Arg Trp Val
180                                         -20
182 gta gca atg ttg gca gtg tta ttt tta ttt cct tcg gta gta gtt gca      224
183 Val Ala Met Leu Ala Val Leu Phe Leu Phe Pro Ser Val Val Val Ala
184 -15          -10          -5          -1
186 gat gga ttg aac ggt acg atg atg cag tat tat gag tgg cat ttg gaa      272
187 Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu
188 1           5           10          15
190 aac gac ggg cag cat tgg aat cgg ttg cac gat gat gcc gca gct ttg      320
191 Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu
192 20          25          30
194 agt gat gct ggt att aca gct att tgg att ccg cca gcc tac aaa ggt      368
195 Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
196 35          40          45
198 aat agt cag gcg gat gtt ggg tac ggt gca tac gat ctt tat gat tta      416
199 Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
200 50          55          60
202 gga gag ttc aat caa aag ggt act gtt cga acg aaa tac gga act aag      464
203 Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
204 65          70          75          80
206 gca cag ctt gaa cga gct att ggg tcc ctt aaa tct aat gat atc aat      512
207 Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
208 85          90          95
210 gta tac gga gat gtc gtg atg aat cat aaa atg gga gct gat ttt acg      560
211 Val Tyr Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr
212 100         105         110
214 gag gca gtg caa gct gtt caa gta aat cca acg aat cgt tgg cag gat      608
215 Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp
216 115         120         125
218 att tca ggt gcc tac acg att gat gcg tgg acg ggt ttc gac ttt tca      656
219 Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser
220 130         135         140
222 ggg cgt aac aac gcc tat tca gat ttt aag tgg aga tgg ttc cat ttt      704
223 Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
224 145         150         155         160
226 aat ggt gtt gac tgg gat cag cgc tat caa gaa aat cat att ttc cgc      752
227 Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg

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228	165	170	175	
230	ttt gca aat acg aac tgg aac tgg cga gtg gat gaa gag aac ggt aat			800
231	Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn			
232	180	185	190	
234	tat gat tac ctg tta gga tcg aat atc gac ttt agt cat cca gaa gta			848
235	Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val			
236	195	200	205	
238	caa gat gag ttg aag gat tgg ggt agc tgg ttt acc gat gag tta gat			896
239	Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp			
240	210	215	220	
242	ttg gat ggt tat cgt tta gat gct att aaa cat att cca ttc tgg tat			944
243	Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr			
244	225	230	235	240
246	aca tct gat tgg gtt cgg cat cag cgc aac gaa gca gat caa gat tta			992
247	Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu			
248	245	250	255	
250	ttt gtc gta ggg gaa tat tgg aag gat gac gta ggt gct ctc gaa ttt			1040
251	Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe			
252	260	265	270	
254	tat tta gat gaa atg aat tgg gag atg tct cta ttc gat gtt cca ctt			1088
255	Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu			
256	275	280	285	
258	aat tat aat ttt tac cgg gct tca caa caa ggt gga agc tat gat atg			1136
259	Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met			
260	290	295	300	
262	cgt aat att tta cga gga tct tta gta gaa gcg cat ccg atg cat gca			1184
263	Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala			
264	305	310	315	320
266	gtt acg ttt gtt gat aat cat gat act cag cca ggg gag tca tta gag			1232
267	Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu			
268	325	330	335	
270	tca tgg gtt gct gat tgg ttt aag cca ctt gct tat gcg aca att ttg			1280
271	Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu			
272	340	345	350	
274	acg cgt gaa ggt ggt tat cca aat gta ttt tac ggt gat tac tat ggg			1328
275	Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly			
276	355	360	365	
278	att cct aac gat aac att tca gct aaa aaa gat atg att gat gag ctg			1376
279	Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu			
280	370	375	380	
282	ctt gat gca cgt caa aat tac gca tat ggc acg cag cat gac tat ttt			1424
283	Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe			
284	385	390	395	400
286	gat cat tgg gat gtt gta gga tgg act agg gaa gga tct tcc tcc aga			1472
287	Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Arg			
288	405	410	415	
290	cct aat tca ggc ctt gcg act att atg tcg aat gga cct ggt ggt tcc			1520
291	Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser			
292	420	425	430	

VERIFICATION SUMMARY

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